

(1) . GENERAL INFORMATIC

(i) APPLICANT: ZEBEDEE, SUZANNE
INCHAUSPE, GENEVIEVE
NASOFF, MARC S.
PRINCE, ALFRED M.
HELTING, TORSTEN B.
DREVIN, HAKAN
NUNN, MICHAEL F.

(ii) TITLE OF INVENTION: METHODS AND SYSTEMS FOR PRODUCING
RECOMBINANT VIRAL ANTIGENS

(iii) NUMBER OF SEQUENCES: 29

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: James P. Hillman
(B) STREET: 45010 Pawnee Drive
(C) CITY: Fremont
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94539

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy Disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Word Perfect 5.0 Dos Txt

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/931,855
(B) FILING DATE: Sep 16, 1997
(C) CLASSIFICATION: Cl. 424, subcl.192.1, 188.1 and 208.1
(C) CLASSIFICATION: Cl. 435, subcl.5 and Cl.422, subcl. 61
(C) CLASSIFICATION: Cl. 424, subcl.189.1, and 228.1
(C) CLASSIFICATION: Cl. 424, subcl.202.1

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US08/563,733
(B) FILING DATE: 8-NOV-1995
(A) APPLICATION NUMBER: US08/049,531
(B) FILING DATE: 20-APR-1993
(A) APPLICATION NUMBER: US07/344,237
(B) FILING DATE: 26-APR-1989
(A) APPLICATION NUMBER: US07/191,229
(B) FILING DATE: 06-MAY-1988
(A) APPLICATION NUMBER: US07/206,499
(B) FILING DATE: 13-JUN-1988
(A) APPLICATION NUMBER: US07/258,016
(B) FILING DATE: 14-OCT-1988

- (A) APPLICAT N NUMBER: US08/272,271
- (B) FILING DATE: 8-JUL-1994
- (A) APPLICATION NUMBER: US07/616,369
- (B) FILING DATE: 21-NOV-1990
- (A) APPLICATION NUMBER: US07/573,643
- (B) FILING DATE: 27-AUG-1990

(viii) ATTORNEY/AGENT INFORMATION (O):

- (A) NAME: James P. Hillman Esq.
- (B) REGISTRATION NUMBER: 29748
- (C) REFERENCE/DOCKET NUMBER: 55467/69

(ix) TELECOMMUNICATION INFORMATION (O)

- (A) TELEPHONE: (510) 651 3991
- (B) TELEFAX: (510) 651 5991
- (C) TELEX:

(2) INFORMATION FOR SE ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 16-789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
AGGAGGGTTT TTCAT ATG CCA ATC GTG CAG AAC ATC CAG GGG CAA ATG GTA      51
      Met Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val
                        5                      10

CAT CAG GCC ATA TCA CCT AGA ACT TTA AAT GCA TGG GTA AAA GTA GTA      99
His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val
      15                      20                      25

GAA GAG AAG GCT TTC AGC CCA GAA GTG ATA CCC ATG TTT TCA GCA TTA      147
Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
      30                      35                      40

TCA GAA GGA GCC ACC CCA CAA GAT TTA AAC ACC ATG CTA AAC ACA GTG      195
Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val
      45                      50                      55                      60

GGG GGA CAT CAA GCA GCC ATG CAA ATG TTA AAA GAG ACC ATC AAT GAG      243
Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu
      65                      70                      75

GAA GCT GCA GAA TGG GAT AGA GTG CAT CCA GTG CAT GCA GGG CCT ATT      291
Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile
      80                      85                      90

GCA CCA GGC CAG ATG AGA GAA CCA AGG GGA AGT GAC ATA GCA GGA ACT      339
Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr
      95                      100                      105

ACT AGT ACC CTT CAG GAA CAA ATA GGA TGG ATG ACA AAT AAT CCA CCT      387
Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro
      110                      115                      120

ATC CCA GTA GGA GAA ATT TAT AAA AGA TGG ATA ATC CTG GGA TTA AAT      435
Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn
```

125	130	135	140	
AAA ATA GTA AGA ATG TAT AGC CCT ACC AGC ATT CTG GAC ATA AGA CAA				483
Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln	145	150	155	
GGA CCA AAG GAA CCC TTT AGA GAC TAT GTA GAC CGG TTC TAT AAA ACT				531
Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr	160	165	170	
CTA AGA GCC GAG CAA GCT TCA CAG GAG GTA AAA AAT TGG ATG ACA GAA				579
Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu	175	180	185	
ACC TTG TTG GTC CAA AAT GCG AAC CCA GAT TGT AAG ACT ATT TTA AAA				627
Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys	190	195	200	
GCA TTG GGA CCA GCG GCT ACA CTA GAA GAA ATG ATG ACA GCA TGT CAG				675
Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln	205	210	215	220
GGA GTA GGA GGA CCC AAA AAT CAA CAA TTA TTA TCC TTA TGG GGG TGT				723
Gly Val Gly Gly Pro Lys Asn Gln Gln Leu Leu Ser Leu Trp Gly Cys	225	230	235	
AAA GGG AAA CTT GTT TGT TAT ACT TCC GTT AAA TGG AAT GGA CCC GGC				771
Lys Gly Lys Leu Val Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly	240	245	250	
CAT AAG GCA AGA GTT TTG TAA TAA				795
His Lys Ala Arg Val Leu	255			

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His Gln Ala Ile	5	10	15
Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala	20	25	30
Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala	35	40	45
Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln			

Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu
65 70 75 80

Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln
85 90 95

Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu
100 105 110

Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly
115 120 125

Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
130 135 140

Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
145 150 155 160

Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu
165 170 175

Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val
180 185 190

Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro
195 200 205

Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
210 215 220

Pro Lys Asn Gln Gln Leu Leu Ser Leu Trp Gly Cys Lys Gly Lys Leu
225 230 235 240

Val Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly His Lys Ala Arg
245 250 255

Val Leu

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 16-789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGGAGGGTTT TTCAT ATG CCA ATC GTG CAG AAC ATC CAG GGG CAA ATG GTA 51

Met Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val
5 10

CAT CAG GCC ATA TCA CCT AGA ACT TTA AAT GCA TGG GTA AAA GTA GTA	99
His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val	
15 20 25	
GAA GAG AAG GCT TTC AGC CCA GAA GTG ATA CCC ATG TTT TCA GCA TTA	147
Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu	
30 35 40	
TCA GAA GGA GCC ACC CCA CAA GAT TTA AAC ACC ATG CTA AAC ACA GTG	195
Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val	
45 50 55 60	
GGG GGA CAT CAA GCA GCC ATG CAA ATG TTA AAA GAG ACC ATC AAT GAG	243
Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu	
65 70 75	
GAA GCT GCA GAA TGG GAT AGA GTG CAT CCA GTG CAT GCA GGG CCT ATT	291
Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile	
80 85 90	
GCA CCA GGC CAG ATG AGA GAA CCA AGG GGA AGT GAC ATA GCA GGA ACT	339
Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr	
95 100 105	
ACT AGT ACC CTT CAG GAA CAA ATA GGA TGG ATG ACA AAT AAT CCA CCT	387
Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro	
110 115 120	
ATC CCA GTA GGA GAA ATT TAT AAA AGA TGG ATA ATC CTG GGA TTA AAT	435
Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn	
125 130 135 140	
AAA ATA GTA AGA ATG TAT AGC CCT ACC AGC ATT CTG GAC ATA AGA CAA	483
Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln	
145 150 155	
GGA CCA AAG GAA CCC TTT AGA GAC TAT GTA GAC CGG TTC TAT AAA ACT	531
Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr	
160 165 170	
CTA AGA GCC GAG CAA GCT TCA CAG GAG GTA AAA AAT TGG ATG ACA GAA	579
Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu	
175 180 185	
ACC TTG TTG GTC CAA AAT GCG AAC CCA GAT TGT AAG ACT ATT TTA AAA	627
Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys	
190 195 200	
GCA TTG GGA CCA GCG GCT ACA CTA GAA GAA ATG ATG ACA GCA TGT CAG	675

Ala	Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln	
205					210					215					220	
GGA	GTA	GGA	GGA	CCC	AAA	AAT	CAA	CAA	AGA	TTA	AAT	TTA	TGG	GGG	TGT	723
Gly	Val	Gly	Gly	Pro	Lys	Asn	Gln	Gln	Arg	Leu	Asn	Leu	Trp	Gly	Cys	
				225					230					235		
AAA	GGG	AAA	CTT	ATT	TGT	TAT	ACT	TCC	GTT	AAA	TGG	AAT	GGA	CCC	GGC	771
Lys	Gly	Lys	Leu	Ile	Cys	Tyr	Thr	Ser	Val	Lys	Trp	Asn	Gly	Pro	Gly	
			240					245					250			
CAT	AAG	GCA	AGA	GTT	TTG	TAA	TAA									795
His	Lys	Ala	Arg	Val	Leu											

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Pro	Ile	Val	Gln	Asn	Ile	Gln	Gly	Gln	Met	Val	His	Gln	Ala	Ile	
				5				10						15		
Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val	Glu	Glu	Lys	Ala	
			20					25					30			
Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser	Glu	Gly	Ala	
			35				40					45				
Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln	
			50			55					60					
Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu	
					70					75					80	
Trp	Asp	Arg	Val	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala	Pro	Gly	Gln	
				85					90					95		
Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr	Thr	Ser	Thr	Leu	
			100					105					110			
Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	Asn	Asn	Pro	Pro	Ile	Pro	Val	Gly	
			115				120					125				
Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn	Lys	Ile	Val	Arg	
			130			135					140					
Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg	Gln	Gly	Pro	Lys	Glu	
					150					155					160	
Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys	Thr	Leu	Arg	Ala	Glu	
				165					170					175		
Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Glu	Thr	Leu	Leu	Val	
			180					185						190		

Gln	Asn	Ala	Asn	Pro	Asp	's	Lys	Thr	Ile	Leu	Lys	Ala	Leu	Gly	Pro
		195					200					205			
Ala	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln	Gly	Val	Gly	Gly
	210					215					220				
Pro	Lys	Asn	Gln	Gln	Arg	Leu	Asn	Leu	Trp	Gly	Cys	Lys	Gly	Lys	Leu
225					230					235					240
Ile	Cys	Tyr	Thr	Ser	Val	Lys	Trp	Asn	Gly	Pro	Gly	His	Lys	Ala	Arg
				245					250					255	
Val	Leu														

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 16-789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGGAGGGTTT TTCAT ATG CCA ATC GTG CAG AAC ATC CAG GGG CAA ATG GTA	51
Met Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val	
5 10	
CAT CAG GCC ATA TCA CCT AGA ACT TTA AAT GCA TGG GTA AAA GTA GTA	99
His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val	
15 20 25	
GAA GAG AAG GCT TTC AGC CCA GAA GTG ATA CCC ATG TTT TCA GCA TTA	147
Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu	
30 35 40	
TCA GAA GGA GCC ACC CCA CAA GAT TTA AAC ACC ATG CTA AAC ACA GTG	195
Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val	
45 50 55 60	
GGG GGA CAT CAA GCA GCC ATG CAA ATG TTA AAA GAG ACC ATC AAT GAG	243
Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu	
65 70 75	
GAA GCT GCA GAA TGG GAT AGA GTG CAT CCA GTG CAT GCA GGG CCT ATT	291
Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile	
80 85 90	

GCA CCA GGC CAG ATG AGA AA CCA AGG GGA AGT GAC AT.. GCA GGA ACT	339
Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr	
95 100 105	
ACT AGT ACC CTT CAG GAA CAA ATA GGA TGG ATG ACA AAT AAT CCA CCT	387
Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro	
110 115 120	
ATC CCA GTA GGA GAA ATT TAT AAA AGA TGG ATA ATC CTG GGA TTA AAT	435
Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn	
125 130 135 140	
AAA ATA GTA AGA ATG TAT AGC CCT ACC AGC ATT CTG GAC ATA AGA CAA	483
Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln	
145 150 155	
GGA CCA AAG GAA CCC TTT AGA GAC TAT GTA GAC CGG TTC TAT AAA ACT	531
Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr	
160 165 170	
CTA AGA GCC GAG CAA GCT TCA CAG GAG GTA AAA AAT TGG ATG ACA GAA	579
Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu	
175 180 185	
ACC TTG TTG GTC CAA AAT GCG AAC CCA GAT TGT AAG ACT ATT TTA AAA	627
Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys	
190 195 200	
GCA TTG GGA CCA GCG GCT ACA CTA GAA GAA ATG ATG ACA GCA TGT CAG	675
Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln	
205 210 215 220	
GGA GTA GGA GGA CCA CAA AAT CAA CAA CTT TTA AAT TTA TGG GGG TGT	723
Gly Val Gly Gly Pro Gln Asn Gln Gln Leu Leu Asn Leu Trp Gly Cys	
225 230 235	
AGA GGG AAA GCT ATT TGT TAT ACT TCC GTT CAA TGG AAT GGA CCC GGC	771
Arg Gly Lys Ala Ile Cys Tyr Thr Ser Val Gln Trp Asn Gly Pro Gly	
240 245 250	
CAT AAG GCA AGA GTT TTG TAA TAA 795	
His Lys Ala Arg Val Leu	
255	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Pro	Ile	Val	Gln	Asn	Ile	Gln	Gly	Gln	Met	Val	His	Gln	Ala	Ile	5	10	15
Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val	Glu	Glu	Lys	Ala	20	25	30
Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser	Glu	Gly	Ala	35	40	45
Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln	50	55	60
Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu	65	70	75
Trp	Asp	Arg	Val	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala	Pro	Gly	Gln	85	90	95
Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr	Thr	Ser	Thr	Leu	100	105	110
Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	Asn	Asn	Pro	Pro	Ile	Pro	Val	Gly	115	120	125
Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn	Lys	Ile	Val	Arg	130	135	140
Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg	Gln	Gly	Pro	Lys	Glu	145	150	155
Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys	Thr	Leu	Arg	Ala	Glu	165	170	175
Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Glu	Thr	Leu	Leu	Val	180	185	190
Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Lys	Ala	Leu	Gly	Pro	195	200	205
Ala	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln	Gly	Val	Gly	Gly	210	215	220
Pro	Gln	Asn	Gln	Gln	Leu	Leu	Asn	Leu	Trp	Gly	Cys	Arg	Gly	Lys	Ala	225	230	235
Ile	Cys	Tyr	Thr	Ser	Val	Gln	Trp	Asn	Gly	Pro	Gly	His	Lys	Ala	Arg	245	250	255

Val Leu

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 16-375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
AGGAGGGTTT TTCAT ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA      51
      Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys
                        5                      10

CGT AAC ACC AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGT GGC GGT      99
Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
      15                      20                      25

CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGA TTG      147
Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu
      30                      35                      40

GGT GTG CGC GCG ACG AGG AAG ACT TCC GAG CGG TCG CAA CCT CGA GGT      195
Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly
      45                      50                      55                      60

AGA CGT CAG CCT ATC CCC AAG GTG CGT CGG CCG GAG GGC AGG ACC TGG      243
Arg Arg Gln Pro Ile Pro Lys Val Arg Arg Pro Glu Gly Arg Thr Trp
                        65                      70                      75

GCT CAG CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGT TGC GGG      291
Ala Gln Pro Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly
                        80                      85                      90

TGG GCG GGA TGG CTC CTG TCT CCC CGT GGC TCT CGG CCT AGC TGG GGC      339
Trp Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly
      95                      100                      105

CCC ACA GAC CCC CGG CGT AGG TCG CGC AAT TTG GGT TAA      378
Pro Thr Asp Pro Arg Arg Arg Ser Arg Asn Leu Gly
      110                      115                      120
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
      5                      10                      15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
      20                      25                      30
```

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly al Arg Ala
 35 40 45
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60
 Ile Pro Lys Val Arg Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly
 65 70 75 80
 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
 85 90 95
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly
 115 120

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 16-375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGGAGGGTTT TTCAT ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA	51
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys	
5 10	
CGT AAC ACC AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGT GGC GGT	99
Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly	
15 20 25	
CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGA TTG	147
Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu	
30 35 40	
GGT GTG CGC GCG ACG AGG AAG ACT TCC GAG CGG TCG CAA CCT CGA GGT	195
Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly	
45 50 55 60	
AGA CGT CAG CCT ATC CCC AAG GCA CGT CGG CCC GAG GGC AGG ACC TGG	243
Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp	
65 70 75	
GCT CAG CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGT TGC GGG	291

Ala Gln Pro Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly
80 85 90

TGG GCG GGA TGG CTC CTG TCT CCC CGT GGC TCT CGG CCT AGC TGG GGC 339

Trp Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly
95 100 105

CCC ACA GAC CCC CGG CGT AGG TCG CGC AAT TTG GGT TAA 378
Pro Thr Asp Pro Arg Arg Ser Arg Asn Leu Gly
110 115 120

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60

Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
100 105 110

Arg Arg Arg Ser Arg Asn Leu Gly
115 120

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(ix) FEATURE:

(A) NAME/KE' CDS
(B) LOCATION: 16-375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
AGGAGGGTTT TTCAT ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA      51
      Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys
                        5                      10

CGT AAC ACC AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGT GGC GGT      99
Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
      15                      20                      25

CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGA TTG      147
Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu
      30                      35                      40

GGT GTG CGC GCG ACG AGG AAG ACT TCC GAG CGG TCG CAA CCT CGA GGT      195
Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly
      45                      50                      55                      60

AGA CGT CAG CCT ATC CCC AAG GAC CGT CGG TCC ACG GGC AAG TCC TGG      243
Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp
      65                      70                      75

GGT AAG CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGT TGC GGG      291
Gly Lys Pro Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly
      80                      85                      90

TGG GCG GGA TGG CTC CTG TCT CCC CGT GGC TCT CGG CCT AGC TGG GGC      339
Trp Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly
      95                      100                      105

CCC ACA GAC CCC CGG CGT AGG TCG CGC AAT TTG GGT TAA      378
Pro Thr Asp Pro Arg Arg Arg Ser Arg Asn Leu Gly
      110                      115                      120
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
                        5                      10                      15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
      20                      25                      30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
```


Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly		
			80					85					90				
TGG	GCG	GGA	TGG	CTC	CTG	TCT	CCC	CGT	GGC	TCT	CGG	CCT	AGC	TGG	GGC	339	
Trp	Ala	Gly	Trp	Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly		
		95					100					105					
CCC	ACA	GAC	CCC	CGG	CGT	AGG	TCG	CGC	AAT	TTG	GGT	TAA	378				
Pro	Thr	Asp	Pro	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly						
		110				115					120						

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn		
				5					10					15			
Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly		
			20					25					30				
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala		
			35				40					45					
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro		
			50			55					60						
Ile	Pro	Lys	Ala	Arg	Arg	Ser	Glu	Gly	Arg	Ser	Trp	Ala	Gln	Pro	Gly		
					70					75					80		
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp		
				85				90						95			
Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Thr	Asp	Pro		
			100					105					110				
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly										
							120										

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(ix) FEATURE:

- (A) NAME/KEY: CDS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGGAGGGTTT TTCAT ATG CCT ATT CAT CAT CAT CAT CAT GGC CCG GGC 51

Met Pro Ile His His His His His His Gly Pro Gly
5 10

TCC GTC ACT GTG TCC CAT CCT AAC ATC GAG GAG GTT GCT CTG TCC ACC 99

Ser Val Thr Val Ser His Pro Asn Ile Glu Glu Val Ala Leu Ser Thr
15 20 25

ACC GGA GAG ATC CCC TTT TAC GGC AAG GCT ATC CCC CTC GAG GTG ATC 147

Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu Val Ile
30 35 40

AAG GGG GGA AGA CAT CTC ATC TTC TGC CAC TCA AAG AAG AAG TGC GAC 195

Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp
45 50 55 60

GAG CTC GCC GCG AAG CTG GTC GCA TTG GGC ATC AAT GCC GTG GCC TAC 243

Glu Leu Ala Ala Lys Leu Val Ala Leu Gly Ile Asn Ala Val Ala Tyr
65 70 75

TAC CGC GGT CTT GAC GTG TCT GTC ATC CCG ACC AGC GGC GAT GTT GTC 291

Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val Val
80 85 90

GTC GTG TCA ACC GAT GCT CTC ATG ACT GGC TTT ACC GGC GAC TTC GAC 339

Val Val Ser Thr Asp Ala Leu Met Thr Gly Phe Thr Gly Asp Phe Asp
95 100 105

TCG GTG ATA GAC TGC AAT ACG GGT ACC GAG CTC GAA TTC TAA 381

Ser Val Ile Asp Cys Asn Thr Gly Thr Glu Leu Glu Phe
110 115 120

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Pro Ile His His His His His His Gly Pro Gly Ser Val Thr Val
5 10 15

Ser His Pro Asn Ile Glu Glu Val Ala Leu Ser Thr Thr Gly Glu Ile
20 25 30

Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu Val Ile Lys Gly Gly Arg
35 40 45

His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala

Lys Leu Val Ala Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu
 65 70 75 80
 Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val Val Val Val Ser Thr
 85 90 95
 Asp Ala Leu Met Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Ile Asp
 100 105 110
 Cys Asn Thr Gly Thr Glu Leu Glu Phe
 115 120

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 16-771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGGAGGGTTT TTCAT ATG TCC CCT ATA CTA GGT TAT TGG AAA ATT AAG GGC 51
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly
 5 10
 CTT GTG CAA CCC ACT CGA CTT CTT TTG GAA TAT CTT GAA GAA AAA TAT 99
 Leu Val Gln Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr
 15 20 25
 GAA GAG CAT TTG TAT GAG CGC GAT GAA GGT GAT AAA TGG CGA AAC AAA 147
 Glu Glu His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys
 30 35 40
 AAG TTT GAA TTG GGT TTG GAG TTT CCC AAT CTT CCT TAT TAT ATT GAT 195
 Lys Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp
 45 50 55 60
 GGT GAT GTT AAA TTA ACA CAG TCT ATG GCC ATC ATA CGT TAT ATA GCT 243
 Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala
 65 70 75
 GAC AAG CAC AAC ATG TTG GGT GGT TGT CCA AAA GAG CGT GCA GAG ATT 291
 Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile
 80 85 90

TCA ATG CTT GAA GGA GCC TT TTG GAT ATT AGA TAC GC GTT TCG AGA 339
 Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg
 95 100 105
 ATT GCA TAT AGT AAA GAC TTT GAA ACT CTC AAA GTT GAT TTT CTT AGC 387
 Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser
 110 115 120
 AAG CTA CCT GAA ATG CTG AAA ATG TTC GAA GAT CGT TTA TGT CAT AAA 435
 Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys
 125 130 135 140
 ACA TAT TTA AAT GGT GAT CAT GTA ACC CAT CCT GAC TTC ATG TTG TAT 483
 Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr
 145 150 155
 GAC GCT CTT GAT GTT GTT TTA TAC ATG GAC CCA ATG TGC CTG GAT GCG 531
 Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala
 160 165 170
 TTC CCA AAA TTA GTT TGT TTT AAA AAA CGT ATT GAA GCT ATC CCA CAA 579
 Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln
 175 180 185
 ATT GAT AAG TAC TTG AAA TCC AGC AAG TAT ATA GCA TGG CCT TTG CAG 627
 Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln
 190 195 200
 GGC TGG CAA GCC ACG TTT GGT GGT GGC GAC CAT CCT CCA AAA TCG GAT 675
 Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp
 205 210 215 220
 CTG GTT CCG CGT GGA TCC GAC GTC AAG TTC CCG GGT GGC GGT CAG ATC 723
 Leu Val Pro Arg Gly Ser Asp Val Lys Phe Pro Gly Gly Gly Gln Ile
 225 230 235
 GTT GGT GGA GTT TAC TTG TTG CCG CGC AGG GAA TTC ATC GTG ACT GAC 771
 Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Glu Phe Ile Val Thr Asp
 240 245 250
 TGA 774

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro

5					10					15					
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu
		20						25					30		
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
		35					40					45			
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
	50					55					60				
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
65					70					75					80
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
				85					90					95	
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
			100					105					110		
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
		115					120					125			
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn
	130					135					140				
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
145					150					155					160
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
				165					170					175	
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
			180					185					190		
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala
		195					200					205			
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg
	210					215					220				
Gly	Ser	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly	Gly	Val
225					230					235					240
Tyr	Leu	Leu	Pro	Arg	Arg	Glu	Phe	Ile	Val	Thr	Asp				
			245						250						

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCAAAATTAC CATATGCCAA TGCAGAA C 31

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GACCCGGCCA TAAGGCAAGA GTTTTGTAAT AAG 33

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: yes
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GATCCTTATT ACAAACTCT TGCCTTATGG CCGG 34

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCTCGCATAT GAGCACGATT CCCAAACC 28

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GACGAATTCT TAACCCAAAT TGC GCGACCT AC 32

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GATCCGACGT CAAGTTCCCG GGTGGCGGTC AGATCGTTGG TGGAGTTTAC TTGTTGCCGC 60

GCAGGG 66

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AATTCCCTGC GCGGCAACAA GTAAACTCCA CCAACGATCT GACCGCCACC CGGGAAGTTG 60

ACGTCG 66

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGAATTCCAT ATGTCCCCTA TACTAGGT 28

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CGGAATTCTC ACCTGCGCGG CAACAA 26

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TATGCCTATT CATCATCATC ATCATCATGG CCCGGAATT CTAAGTAAGT AG 52

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCCTACTT ACTTAGAATT CCCGGGCCAT GATGATGATG ATGATGAATA GGCA 54
^Z